

STEVEN M. FOLTZ

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EDUCATION

PhD, Washington University in St. Louis, St. Louis, MO June 2014 – March 2020

Division of Biology and Biomedical Sciences (DBBS) Human and Statistical Genetics Program
Precision Medicine Pathway

Advisor: Li Ding, PhD

Thesis: Multi-omics integration for gene fusion discovery and somatic mutation haplotyping in cancer

MS Biostatistics, University of Washington, Seattle, WA September 2011 – August 2013

Advisors: Brian Browning, PhD, and Sharon Browning, PhD

Thesis: Rare variant method for identity-by-descent detection in sequence data, and the time to most recent common ancestor given identity-by-descent segment length

BS Mathematics, Presbyterian College, Clinton, SC August 2006 – May 2010

Advisor: Doug Daniel, PhD

Thesis: Tiling 2-deficient Rectangles with Trominoes

RESEARCH EXPERIENCE

Washington University in St. Louis, St. Louis, MO June 2014 – May 2020

Graduate student, Laboratory of Li Ding, PhD

Thesis: Multi-omics integration for gene fusion discovery and somatic mutation haplotyping in cancer

- Pan-cancer computational projects utilizing tumor and normal tissue sequencing data to understand patterns of germline and somatic variation
- Integrative data analysis tool and pipeline development, including variant calling and quality control using bulk DNA and RNA, single-cell RNA, and linked-read DNA sequencing
- Gene fusion discovery from The Cancer Genome Atlas (9,624 patients, 33 cancer types) and a large multiple myeloma cohort (742 patients), highlighting clinically-relevant events
- Linked-read whole genome sequencing data analysis for phasing somatic mutations, understanding haplotype structures, and modeling tumor evolution
- Led research conference calls with TCGA and other collaborators to drive projects to successful completion

- Organized and delivered donor presentations to establish lab funding through the Riney Blood Cancer Initiative (\$25 million since Fall 2017)

My work has led to two first author papers published in *Bioinformatics* and *Cell Reports*, one accepted in *Nature Communications*, one under review, and one in preparation. Additionally, I am co-author on four papers published in *Cell*, *Nature Medicine*, *Molecular Psychiatry*, and *Annals of Oncology*.

Virginia Commonwealth University, Richmond, VA

August 2013 – May 2014

Biostatistician, Laboratory of Nengliang Yao, PhD

- Led statistical aspects of cancer care research as part of a healthcare policy team
- Procured, cleaned, and analyzed data from national cancer databases, including SEER
- Developed geographically weighted regression and spatial panel data models

This work led to a co-author publication in *PLOS One*.

University of Washington, Seattle, WA

September 2011 – August 2013

Graduate research assistant, Laboratory of Brian Browning, PhD, and Sharon Browning, PhD

Thesis: Rare variant method for identity-by-descent detection in sequence data, and the time to most recent common ancestor given identity-by-descent segment length

- Implemented novel algorithms to define identity-by-descent (IBD) between individuals using rare DNA variation and developed statistical models for shared ancestor inference
- Worked with data from the 1000 Genomes Project and simulated coalescent model data
- Assisted in methods development for missing data imputation and haplotype phasing

Presbyterian College, Clinton, SC

Spring 2010

Undergraduate research in mathematics, advised by Doug Daniel, PhD

Thesis: Tiling 2-deficient Rectangles with Trominoes

- Developed analytical and computational approaches to answer an open question about tiling deficient rectangular fields with trominoes

Medical University of South Carolina, Charleston, SC

Summer 2009

Undergraduate Summer Research Fellow, Laboratory of Jim Zheng, PhD

- Created a weighted clustering coefficient model to detect regions of high interconnectivity in yeast gene networks based on synthetic lethal interactions

Presbyterian College, Clinton, SC

Fall 2008 – Spring 2009

Undergraduate research assistant, Laboratory of James Wanliss, PhD

- Analyzed space weather data to refine solar storm prediction models

PUBLICATIONS

1. **Foltz, S. M.**, *et al.* Linked-read sequencing reveals haplotypes and phasing of somatic variants in multiple myeloma. (In preparation, submission March 2020)
2. Liu, R.*, Q. Gao*, **S. M. Foltz***, *et al.* Co-evolution of tumor and immune cells during progression of multiple myeloma. *Authors contributed equally. (Submitted, *Nature Cancer*)
3. **Foltz, S. M.**, *et al.* Evolution and structure of clinically relevant gene fusions in multiple myeloma. (Accepted, *Nature Communications*)
4. Sanchez-Vega, F., M. Mina, J. Armenia, W. K. Chatila, A. Luna, K. C. La, S. Dimitriadou, D. L. Liu, H. S. Kantheti, S. Saghafeinia, D. Chakravarty, F. Daian, Q. Gao, M. H. Bailey, W. W. Liang, **S. M. Foltz**, I. Shmulevich, L. Ding, Z. Heins, A. Ochoa, B. Gross, J. Gao, H. Zhang, R. Kundra, C. Kandoth, I. Bahceci, L. Dervishi, U. Dogrusoz, W. Zhou, H. Shen, P. W. Laird, G. P. Way, C. S. Greene, H. Liang, Y. Xiao, C. Wang, A. Iavarone, A. H. Berger, T. G. Bivona, A. J. Lazar, G. D. Hammer, T. Giordano, L. N. Kwong, G. McArthur, C. Huang, A. D. Tward, M. J. Frederick, F. McCormick, M. Meyerson, Cancer Genome Atlas Research Network, E. M. Van Allen, A. D. Cherniack, G. Ciriello, C. Sander and N. Schultz (2018). Oncogenic Signaling Pathways in The Cancer Genome Atlas. *Cell* **173**(2): 321-337 e310
5. Gao, Q.*, W. W. Liang*, **S. M. Foltz***, G. Mutharasu, R. G. Jayasinghe, S. Cao, W. W. Liao, S. M. Reynolds, M. A. Wyczalkowski, L. Yao, L. Yu, S. Q. Sun, Fusion Analysis Working Group, Cancer Genome Atlas Research Network, K. Chen, A. J. Lazar, R. C. Fields, M. C. Wendl, B. A. Van Tine, R. Vij, F. Chen, M. Nykter, I. Shmulevich and L. Ding (2018). Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. *Cell Rep* **23**(1): 227-238 e223. *Authors contributed equally.
6. **Foltz, S. M.**, W. W. Liang, M. Xie and L. Ding (2017). MIRMMR: binary classification of microsatellite instability using methylation and mutations. *Bioinformatics* **33**(23): 3799-3801
7. Dang, H. X., B. S. White, **S. M. Foltz**, C. A. Miller, J. Luo, R. C. Fields and C. A. Maher (2017). ClonEvol: clonal ordering and visualization in cancer sequencing. *Ann Oncol* **28**(12): 3076-3082
8. Ye, K., J. Wang, R. Jayasinghe, E. W. Lameijer, J. F. McMichael, J. Ning, M. D. McLellan, M. Xie, S. Cao, V. Yellapantula, K. L. Huang, A. Scott, **S. Foltz**, B. Niu, K. J. Johnson, M. Moed, P. E. Slagboom, F. Chen, M. C. Wendl and L. Ding (2016). Systematic discovery of complex insertions and deletions in human cancers. *Nat Med* **22**(1): 97-104
9. Olfson, E., N. L. Saccone, E. O. Johnson, L. S. Chen, R. Culverhouse, K. Doheny, **S. M. Foltz**, L. Fox, S. M. Gogarten, S. Hartz, K. Hetrick, C. C. Laurie, B. Marosy, N. Amin, D. Arnett, R. G. Barr, T. M. Bartz, S. Bertelsen, I. B. Borecki, M. R. Brown, D. I. Chasman, C. M. van Duijn, M. F. Feitosa, E. R. Fox, N. Franceschini, O. H. Franco, M. L. Grove, X. Guo, A. Hofman, S. L. Kardina, A. C. Morrison, S. K. Musani, B. M. Psaty, D. C. Rao, A. P. Reiner, K. Rice, P. M. Ridker, L. M. Rose, U. M. Schick, K. Schwander, A. G. Uitterlinden, D. Vojinovic, J. C. Wang, E. B. Ware, G. Wilson, J. Yao, W. Zhao, N. Breslau, D. Hatsukami, J. A. Stitzel, J. Rice, A. Goate and L. J. Bierut (2016). Rare, low frequency and common coding variants in *CHRNA5* and their contribution to nicotine dependence in European and African Americans. *Mol Psychiatry* **21**(5): 601-607

10. Yao, N., **S. M. Foltz**, A. Y. Odisho and D. C. Wheeler (2015). Geographic analysis of urologist density and prostate cancer mortality in the United States. *PLOS One* **10**(6): e0131578
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TEACHING EXPERIENCE

Washington University in St. Louis, St. Louis, MO

Instructor, Introduction to Python – Bioinformatics Winter 2019

Student profile: 6 post-baccalaureate students from the Opportunities in Genomics Research diversity outreach program.

Responsibilities: Developed syllabus, created course content, led weekly classroom lectures and activities, gathered regular student feedback.

Teaching assistant, Genomics (Biol 5488) Spring 2016

Student profile: 40 first-year graduate students from different biomedical programs and with a wide range of programming experience.

Responsibilities: Taught scientific and computational concepts for weekly programming labs (Python), hosted office hours, evaluated student performance on labs and exams (one of four TAs).

Tutor, Fundamentals of Biostatistics for Graduate Students (Biol 5075) Fall 2015, Fall 2016

Student profile: 30 first-year graduate students mostly lacking computational experience.

Responsibilities: Taught background bioinformatics and computer coding skills (Python) for programming lab assignments.

Presbyterian College, Clinton, SC

Tutor, Department of Mathematics January 2007 – April 2010

Student profile: Individuals or groups of undergraduate students from courses up to Calculus II needing help with problem sets and test preparation.

Responsibilities: Re-taught core mathematics concepts in an applied way to bridge gaps in each student's understanding.

MENTORING EXPERIENCE

Mentoring for Ding Lab rotation graduate students

- Yize Li (Fall 2017)
Current status: joined the lab
Copy number variation quality control pipeline
- Ruiyang Liu (Fall 2017)
Current status: joined the lab
Cell type decomposition from bulk RNA-seq

- Lijun Yao (Fall 2017)
Current status: joined the lab
Fusion gene quality control metrics and driver fusion methods

Mentoring for Ding Lab undergraduate students

* Undergraduates to be included as co-authors on research papers

- * Moses Schindler (Summer – Fall 2019)
Current status: Washington University in St. Louis, Class of 2023
Tumor evolution modeling and graph-based methods using single cell RNA-seq
- * Jessika Baral (Fall 2018)
Current status: Washington University in St. Louis, Class of 2021
Haplotype and variant data analysis from 1000 Genomes
- * Guanlan Dong (Fall 2018, Spring 2019)
Graduated Washington University in St. Louis: Spring 2019
Current status: graduate student at Harvard University
Haplotype phase sets and genome assembly summarization
- * Justin Chen (Summer 2018)
Current status: Columbia University, Class of 2022
Multiple myeloma phased and unphased variant comparison
- Edwin Qiu (Spring 2018, Fall 2018)
Current status: Washington University in St. Louis, Class of 2020
Driver fusion prioritization methods development

Mentoring for Washington University Young Scientist Program high schoolers

- Jada Reid (Fall 2014 – Spring 2018)
Graduated Collegiate School of Medicine and Bioscience: Spring 2018
Current status: Wesleyan University, Class of 2022

PRESENTATIONS

Oral presentations

- “Multiple Myeloma: Groundbreaking DNA, RNA, and protein technologies at WashU.” Washington University School of Medicine Paula C. and Rodger O. Riney Blood Cancer Research Initiative Advisory Board Meeting. February 2019.
- “RNA-Seq and fusion discovery pipeline for a large multiple myeloma cohort.” WashU DBBS Precision Medicine Pathway Retreat. October 2017.

- “RNA and DNA methylation signatures for scoring tumor stemness.” WashU DBBS Precision Medicine Pathway Retreat. September 2016.

Poster presentations

- “Fusion gene detection across a large cohort of multiple myeloma patients.” International Myeloma Workshop. Boston, MA. September 2019.
- “Comprehensive Multi-Omics Analysis of Gene Fusions in a Large Multiple Myeloma Cohort.” American Society of Hematology. San Diego, CA. December 2018.
- “Multiple Myeloma RNA-seq and Fusion Discovery Pipeline.” WashU DBBS Computational and Systems Biology / Human and Statistical Genetics / Molecular Genetics and Genomics Joint Program Retreat. Potosi, MO. September 2017.
- “Genomic region and sample selection strategy for variant discovery and association analysis.” Genome Informatics. Cold Spring Harbor, NY. October 2015.
- “Comprehensive Analysis of Germline Complex Insertions and Deletions.” WashU DBBS Computational and Systems Biology / Molecular Genetics and Genomics Joint Program Retreat. New Haven, MO. September 2015.
- “Comprehensive Analysis of Germline Complex Insertions and Deletions.” WashU DBBS Human and Statistical Genetics Program Retreat. St. Louis, MO. September 2015.
- “Identity-by-descent analysis of sequence data.” International Genetic Epidemiology Society. Stevenson, WA. October 2012.

RESEARCH SKILLS

- Computational and data analysis project management and team leadership
- Multi-institutional collaborations, e.g. The Cancer Genome Atlas (TCGA), Clinical Proteomic Tumor Analysis Consortium (CPTAC), Multiple Myeloma Research Foundation (MMRF)
- Analysis of large-scale sequencing data (DNA, RNA) and file formats (VCF, BAM, MAF, BED) on large Unix clusters
- Cancer bioinformatics tools: fusion detection, copy number detection, gene expression, clonal evolution modeling
- Programming languages: R, Python, Bash, Unix command line (github.com/envest)
- Data presentation tools: ggplot2 (R package), Adobe Illustrator and InDesign, \LaTeX
- Statistical modeling, including survival analysis

PROFESSIONAL DEVELOPMENT

The Teaching Center at Washington University in St. Louis Fall 2014 – January 2020
Professional Development in Teaching Program

- Preparation in Pedagogy (PiP)
 - Foundational and advanced level teaching workshops
 - Qualifying teaching experience
 - Teaching Philosophy Statement
- WU-CIRTL “Practitioner” level
 - Completed PiP and Scholarship of Teaching and Learning course

Center for the Integration of Research, Teaching, and Learning (CIRTL)
National CIRTL Forum, Drexel University, Philadelphia, PA October 13-15, 2019

Center for the Improvement of Mentored Experience in Research (CIMER)
Mentorship Training Program, WashU, St. Louis, MO April 1-2, 2019

Science Education Partnership and Assessment Laboratory (SEPAL @SFSU)
Evidence-based Teaching for Researchers, WashU, St. Louis, MO September 21, 2018

Midstates Consortium for Mathematics and Science July 6-8, 2018
Early Career Workshop, Gustavus Adolphus College, St. Peter, MN

HONORS AND AWARDS

- “Best of *Cell Reports* 2018” – co-first author of a frequently cited publication (Driver Fusions and Their Implications in the Development and Treatment of Human Cancers).
- “Outstanding Mentor” – recognizing one mentor working with high schoolers through the Washington University Young Scientist Program (25th Anniversary Gala, October 22, 2016).
- “Outstanding Senior in Mathematics” – awarded to the top graduating senior in the department (Presbyterian College Honors Convocation, April 15, 2010).

SERVICE AND OUTREACH

Young Scientist Program, Washington University in St. Louis, St. Louis, MO
Leader of Mentoring Program Cohort Fall 2014 – Spring 2018

- Led 12 graduate students paired with high schoolers for four years

- Coordinated bi-weekly school visits and educational field trips
- Facilitated lesson planning and resources available for hands on science activities
- Mentored one student (Jada Reid, Wesleyan University, Class of 2022)

St. Louis Science Center, St. Louis, MO

Summer 2015

Exhibit interpreter

- Smithsonian and NHGRI sponsored exhibit Genome: Unlocking Life's Code
- Discussed the science, ethics, and societal impacts of genomics with museum patrons

GRADUATE SCHOOL COURSEWORK

Washington University in St. Louis, St. Louis, MO

June 2014 – May 2018

Ph.D. Biology and Biomedical Sciences (Human and Statistical Genetics) (GPA: 4.00/4.00)

Human Linkage and Association Analysis; Fundamentals of Mammalian Genetics; Computational Statistical Genetics; Genomics; Human Genetics Journal Club; Genetics and Genomics of Disease; Ethics and Research Science; Communicating Science: Writing for Multiple Audiences; Scholarship of Teaching and Learning

University of Washington, Seattle, WA

September 2011 – August 2013

MS Biostatistics (GPA: 3.43/4.00)

Biostatistics I, II; Statistical Inference I, II; Theory of Linear Models; Statistical Genetics I; Categorical Data Analysis; Survival Data Analysis; Evolutionary Genetics; Population Genetics; Statistical Genetics Seminar; Biostatistics Seminar

OTHER WORK EXPERIENCE

Across, Nairobi, Kenya

August 2010 – July 2011

Institutional and Organizational Development Volunteer

Promoted the organization and its mission (holistic transformation of South Sudan communities) to an international audience through the website and other publications. Key aspects of the organization's mission included: serving refugees and internally displaced persons, promoting gender equity and sustainable agriculture, and training teachers and health care providers. Placement coordinated through the Presbyterian Church (U.S.A.) Young Adult Volunteers program.

Last updated: April 2, 2020